MEDLINE SEARCH FOR "a covalent complex".

L7 ANSWER 150 OF 156 MEDLINE
AN 80101458 MEDLINE
DN 80101458 PubMed ID: 293659
TI Covalent association of protein with replicative form DNA of parvovirus H-1.
AU Revie D; Tseng B Y; Grafstrom R H; Goulian M
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1979 Nov) 76 (11) 5539-43.
Journal code: PV3; 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198003
ED Entered STN: 19900315
Last Updated on STN: 19900315
Entered Medline: 19800317
AB The double-stranded replicative form (RF) DNA of the autonomous parvovirus H-1 can be isolated from infected cells in **a covalent complex** with protein. The protein is present on most or all of the RF DNA, including actively replicating molecules, and is associated with the 5'-terminal endonuclease Hae III fragments of both the viral and complementary strands of RF. The size of the protein is estimated to be 60,000-70,000 daltons from its effect on buoyant density of DNA. DNA with covalently bound protein has not been found in H-1 virions.

L7 ANSWER 151 OF 156 MEDLINE
AN 79083831 MEDLINE
DN 79083831 PubMed ID: 728836
TI Blood replacement in dogs by dextran-hemoglobin.
AU Tam S C; Blumenstein J; Wong J T
SO CANADIAN JOURNAL OF BIOCHEMISTRY, (1978 Oct) 56 (10) 981-4.
Journal code: CHN; 0421034. ISSN: 0008-4018.
CY Canada
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197903
ED Entered STN: 19900314
Last Updated on STN: 19900314
Entered Medline: 19790328
AB Exchange transfusions in dogs were performed with a solution of either dextran or **a covalent complex** between dextran and human hemoglobin. Dogs transfused with dextran alone died when their hematocrit was lowered to 6-10%. Dogs transfused with dextran-hemoglobin complex, however, survived a reduction of their hematocrit to 2% or below. In the latter animals, the dextran-hemoglobin complex disappeared from the circulation with an average half-life of 2.4 days. Correcting for oxidation of the hemoglobin moiety to methemoglobin, the half-life of functional unoxidized dextran-hemoglobin in the circulation was 1.9 days. In compensation for the loss of dextran-hemoglobin, vigorous erythropoiesis was observed at a rate of close to 5% hematocrit per day over the first 2 days following the exchange transfusion. As a result, the total hemoglobin concentration in blood was maintained at 5-6% during this period, and the animals went on to complete recovery in room air without the need for further transfusion with dextran-hemoglobin.

L7 ANSWER 152 OF 156 MEDLINE
AN 79083126 MEDLINE
DN 79083126 PubMed ID: 728540
TI Structural evidence on DNA carcinogen interactions. N-acetoxy-N-2acetylaminofluorene binding to DNA.
AU Norden B
SO BIOPHYSICAL CHEMISTRY, (1978 Sep) 8 (4) 385-91.
Journal code: A5T; 0403171. ISSN: 0301-4622.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197903
ED Entered STN: 19900314
Last Updated on STN: 19900314
Entered Medline: 19790324
AB Linear dichroism (LD) gives useful information on the interaction between DNA and the directly acting carcinogen N-acetoxy-N-2acetylaminofluorene (AAAF). In 50% methanol solvent with low ionic strength only a weak complex (van der Waals) appears. However, above 40 degrees C strand separation takes place and a covalent aminofluorene complex forms. After renaturation a characteristic positive LD band is observed at 306 nm. The average angular orientation of the long-axis of the fluorene moiety (47 degrees to the local helix axis) is inconsistent with intercalation. It can be explained for instance by a free rotation around a C(DNA)-N(aminofluorene) bond or by a major groove site. The occupation density was 1--2 aminofluorene residues per 100 bases. With native DNA, AAAF slowly forms **a covalent complex** which has a negative LD at 307 nm. The orientation (70--90 degrees) is consistent with steric direction by the strand.

L7 ANSWER 153 OF 156 MEDLINE
AN 78214673 MEDLINE
DN 78214673 PubMed ID: 97081
TI Purification and characterization of the penicillin-binding protein that is the lethal target of penicillin in Bacillus megaterium and Bacillus licheniformis. Protein exchange and complex stability.
AU Chase H A; Reynolds P E; Ward J B
SO EUROPEAN JOURNAL OF BIOCHEMISTRY, (1978 Jul 17) 88 (1) 275-85.
Journal code: EMZ; 0107600. ISSN: 0014-2956.
CY GERMANY, WEST: Germany, Federal Republic of
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197809
ED Entered STN: 19900314
Last Updated on STN: 19900314
Entered Medline: 19780929
AB The penicillin-binding protein that is thought to be the lethal target of penicillin in Bacillus megaterium (protein 1) has been purified to greater than 95% homogeneity. The membrane-bound penicillin-binding proteins were solubilized with a non-ionic detergent and partially separated from each other by ion-exchange chromatography on DEAE-Sepharose CL-6B. Protein 1 was subsequently purified by covalent affinity chromatography on ampicillin-affinose. Bacillus licheniformis contains an equivalent penicillin-binding protein (protein 1) that can be more readily purified to virtual homogeneity in a one-step procedure. It was separated from the other penicillin-binding proteins by utilizing the observation that in this organism, this particular protein is the only one whose covalent complex with benzylpenicillin subsequently breaks down. Membranes were treated with saturating concentrations of benzylpenicillin followed by the removal of free penicillin and further incubation to allow the complex between benzylpenicillin and protein 1 to break down. The

penicillin-binding proteins were then solubilized and applied to a column of ampicillin-affinose to which only protein 1 was bound as the other penicillin-binding proteins still had benzylpenicillin bound to them. Pure protein 1 was eluted from the affinity resin with hydroxylamine. The interaction of benzylpenicillin with purified protein 1 has been studied by separating unbound antibiotic from the benzylpenicillin . protein complex by paper electrophoresis. Benzylpenicillin reacts with the protein rapidly to form **a covalent complex** and the fully saturated complex has a molar ratio of bound [14C] benzylpenicillin: protein of 0.7:1. The complex breaks down, obeying first-order kinetics, with a half-life of 16 min at 35 degrees C, a value identical to that obtained with the membrane-bound protein. The concentration of benzylpenicillin that results in the formation of 50% of the maximum amount of benzylpenicillin . protein complex is that at which the molar amount of benzylpenicillin present is equal to 50% of the molar amount of penicillin-binding protein, rather than being a measure of any of the kinetic parameters of the binding reaction. This observation may be significant in the interpretation of previous results where the amounts of penicillins needed to kill cells or to inhibit penicillin-sensitive reactions have been expressed as concentrations. The possible importance of the breakdown of beta-lactam . protein complexes in the clinical use of these antibiotics is discussed.

L7 ANSWER 154 OF 156 MEDLINE
AN 78130039 MEDLINE
DN 78130039 PubMed ID: 204634
TI Interaction of cytochrome c with cytochrome c oxidase. Photoaffinity labeling of beef heart cytochrome c oxidase with arylazido-cytochrome c.
AU Bisson R; Azzi A; Gutweniger H; Colonna R; Montecucco C; Zanotti A
SO JOURNAL OF BIOLOGICAL CHEMISTRY, (1978 Mar 25) 253 (6) 1874-80.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197805
ED Entered STN: 19900314
Last Updated on STN: 19970203
Entered Medline: 19780517
AB Cytochrome c derivatives labeled with a 3-nitrophenylazido group at lysine 13, at lysine 22, or at both residues have been prepared. The interaction of the cytochrome c derivatives with beef heart cytochrome c oxidase (ferrocytochrome c:oxygen oxidoreductase, EC 1.9.3.1) in the presence of ultrviolet light results in formation of **a covalent complex** between cytochrome c and the oxidase. Using the lysine 22 derivative, the polypeptide composition of the oxidase is not modified, nor is its catalytic activity, whereas with the lysine 13 derivative, the gel electrophoretic pattern is altered and the catalytic activity of the complex diminished. The data are consisten with a specfic covalent interaction of the lysine 13 derivative of cytochrome c with the polypeptide of molecular weight 23,700 (Subunit II) of cytochrome c oxidase.

L7 ANSWER 155 OF 156 MEDLINE
AN 76174270 MEDLINE
DN 76174270 PubMed ID: 772423
TI Production of frameshift mutations in Salmonella by a light sensitive azide analog of ethidium.
AU Yielding L W; White W E Jr; Yielding K L
SO MUTATION RESEARCH, (1976 Mar) 34 (3) 351-8.

Journal code: NNA; 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197607
ED Entered STN: 19900313
Last Updated on STN: 19900313
Entered Medline: 19760706
AB Frameshift mutations have been produced in specific repair-negative Salmonella tester strains by photoaffinity labeling technique using ethidium azide. Reversions requiring a +1 addition or a -2 deletion were specially sensitive. Mutagenesis was reduced by the simultaneous addition of non-mutagenic ethidium bromide, and was prevented by photolysis of the azide prior to culture addition. Identical tester strains active in DNA excision repaire were not mutagenized by the azide. These results are consistent with the interpretation that photolysis of the bound ethidium analog converts the drug from its noncovalent mode of binding (presumably intercalation) to **a covalent complex** with consequent production of frameshift mutations. Such photoaffinity labeling by drugs which bind to DNA not only confirms the importance of covalent drug attachment for frameshift mutagenesis, but also provides powerful techniques for studying the molecular deatils of a variety of genetic mechanisms.

L7 ANSWER 156 OF 156 MEDLINE
AN 76161221 MEDLINE
DN 76161221 PubMed ID: 1259963
TI On the individuality of aliphatic and alicyclic monoester lipases in human adipose tissue.
AU Charbonnier M; Boyer J
SO BIOCHIMICA ET BIOPHYSICA ACTA, (1976 Mar 26) 424 (3) 329-36.
Journal code: A0W; 0217513. ISSN: 0006-3002.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197607
ED Entered STN: 19900313
Last Updated on STN: 19970203
Entered Medline: 19760706
AB Aliphatic and alicyclic monoester lipase activities from human adipose tissue have been comparatively investigated by using [3H] oleoylethanol and [14C] oleoylcholesterol, respectively, as substrates. A number of specific properties proved to be different for each activity. Different rates of decay of hydrolytic activity towards each substrate were observed during heat denaturation. Stability upon exposure to the cold was different for both activities, and the protective effect of glycerol was less effective for oleoylcholesterol than for oleoylethanol lipase. Serial (NH4)2SO4 fractionation in 5% increments showed that the two activities did not precipitate at identical saturation values. The behaviours of the two activities were compared in an affinity system where monoolein, a substrate molecule, served as a ligand for the enzyme(s) in **a covalent complex** with CH-Sepharose. During chromatography, both activities followed a comparable adsorption-elution pattern, but the oleoylcholesterol to oleoylethanol lipase activity ratio decreased by a factor of 4. Taken together, these data, along with a differential susceptibility to various surfactants, confirm our earlier hypothesis (Arnaud, J. and Boyer, J (1974) Biochim. Biophys. Acta 337, 165--168) that aliphatic and alicyclic monoester lipase activities in human fat are referable to distinct catalytic proteins.